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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/641,319C

DATE: 08/06/2002

TIME: 17:06:34

Input Set : A:\04578--2.txt

Output Set: N:\CRF3\08062002\I641319C.raw

5 <110> APPLICANT: Slater, Michael
7 Huang, Fen
9 Hartnett, James
13 <120> TITLE OF INVENTION: Mutant TNE Polymerases
17 <130> FILE REFERENCE: PRMG-04578
21 <140> CURRENT APPLICATION NUMBER: 09/641,319C
23 <141> CURRENT FILING DATE: 2000-08-18
27 <150> PRIOR APPLICATION NUMBER: 09/385,986
29 <151> PRIOR FILING DATE: 1999-08-30
33 <150> PRIOR APPLICATION NUMBER: 08/484,661
35 <151> PRIOR FILING DATE: 1995-06-07
39 <160> NUMBER OF SEQ ID NOS: 51
43 <170> SOFTWARE: PatentIn version 3.0
47 <210> SEQ ID NO: 1
49 <211> LENGTH: 2682
51 <212> TYPE: DNA
53 <213> ORGANISM: Thermotoga neapolitana
57 <220> FEATURE:
59 <221> NAME/KEY: CDS
61 <222> LOCATION: (1)..(2679)
65 <400> SEQUENCE: 1

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68 1 5 10 15	
70 tat tac gcc ctc gac aga tcc ctt tcc aca tcc aca gga att cca acg	96
71 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr	
72 20 25 30	
74 aac gcc gtc tat ggc gtt gcc agg atg ctc gtt aaa ttc ata aag gaa	144
75 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu	
76 35 40 45	
78 cac att ata ccc gaa aag gac tac gcg gct gtg gcc ttc gac aag aag	192
79 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys	
80 50 55 60	
82 gca gcg acg ttc aga cac aaa ctg ctc gaa gcg tac aag gcg caa agg	240
83 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg	
84 65 70 75 80	
86 cca aag acg ccg gat ctt cta gtt cag cag cta cct tac atc aag cgg	288
87 Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg	
88 85 90 95	
90 ctg ata gaa gct ctt ggt ttc aaa gtg ctg gag ctg gaa gga tac gaa	336
91 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu	
92 100 105 110	
94 gca gac gat atc atc gcc acg ctt gca gtc aag ggc tgc acg ttt ttt	384

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95 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe
96      115      120      125
98 gat gag att ttc ata ata acc ggt gac aag gat atg ctt caa ctt gta      432
99 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
100      130      135      140
102 aac gag aag ata aag gtc tgg aga atc gtc aag ggg ata tcg gat ctt      480
103 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
104 145      150      155      160
106 gag ctt tac gat tcg aaa aag gtg aaa gaa aga tac ggt gtg gaa cca      528
107 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
108      165      170      175
110 cat cag ata ccg gat ctt cta gca ctg acg gga gac gag ata gac aac      576
111 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn
112      180      185      190
114 att ccc ggt gta acg gga ata ggt gaa aag acc gct gta cag ctt ctc      624
115 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
116      195      200      205
118 ggc aag tac aga aat ctt gaa gac att ctg gag cat gcc cgt gaa ctc      672
119 Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu
120      210      215      220
122 ccc cag aqa gtg aga aag gct ctc ttg aga gac agg gaa gtt gcc atc      720
123 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
124 225      230      235      240
126 ctc agt aaa aaa ctt gca act ctg gtg acg aac gca cct gtt gaa gtg      768
127 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
128      245      250      255
130 gac tgg gaa gag atg aaa tac aga gga tac gac aag aga aaa cta ctt      816
131 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
132      260      265      270
134 ccg ata ttg aaa gaa ctg gag ttt gct tcc atc atg aag gaa ctt caa      864
135 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
136      275      280      285
138 ctg tac gaa gaa gca gaa ccc acc gga tac gaa atc gtg aag gat cat      912
139 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
140      290      295      300
142 aag acc ttc gaa gat ctc atc gaa aag ctg aag gag gtt cca tct ttt      960
143 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
144 305      310      315      320
146 gcc ctg gac ctt gaa acg tcc tcc ctt gac ccg ttc aac tgt gag ata      1008
147 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
148      325      330      335
150 gtc ggc atc tcc gtg tcg ttc aaa ccg aaa aca gct tat tac att cca      1056
151 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
152      340      345      350
154 ctt cat cac aga aac gcc cag aat ctt gat gaa aca ctg gtg ctg tcg      1104
155 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
156      355      360      365
158 aag ttg aaa gag atc ctc gaa gac ccg tct tcg aag att gtg ggt cag      1152
159 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln

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160	370	375	380	
162	aac ctg aag tac gac tac aag gtt ctt atg gta aag ggt ata tcg cca	1200		
163	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro			
164	385 390 395 400			
166	gtt tat ccg cat ttt gac acg atg ata gct gca tat ttg ctg gag cca	1248		
167	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro			
168	405 410 415			
170	aac gag aaa aaa ttc aat ctc gaa gat ctg tct ttg aaa ttt ctc gga	1296		
171	Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly			
172	420 425 430			
174	tac aaa atg acg tct tat cag gaa ctg atg tcg ttt tcc tca cca ctt	1344		
175	Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu			
176	435 440 445			
178	ttt ggt ttc agc ttt gcg gat gtt ccg gta gac aag gct gcg aac tac	1392		
179	Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr			
180	450 455 460			
182	tcc tgc gag gat gca gac atc act tat agg ctc tac aag ata ctc agc	1440		
183	Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser			
184	465 470 475 480			
186	atg aag ctc cat gaa gcg gaa ctt gag aac gtc ttc tac agg ata gag	1488		
187	Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu			
188	485 490 495			
190	atg ccg ctt gtg aac gtt ctt gca cgc atg gaa ttg aac ggg gtg tat	1536		
191	Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr			
192	500 505 510			
194	gtg gac aca gaa ttc ctg aaa aag ctc tcg gag gag tac ggc aaa aag	1584		
195	Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys			
196	515 520 525			
198	ctc gag gaa ctg gcc gaa aaa atc tac cag ata gca gga gag ccc ttc	1632		
199	Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe			
200	530 535 540			
202	aac atc aat tct cca aaa cag gtt tca aag atc ctt ttt gag aag ctg	1680		
203	Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu			
204	545 550 555 560			
206	gga ata aaa ccc cgt gga aaa acg aca aaa aca gga gcg tac tct acc	1728		
207	Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Ala Tyr Ser Thr			
208	565 570 575			
210	agg ata gag gtg ttg gaa gag ata gcg aat gag cac gag ata gta ccc	1776		
211	Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro			
212	580 585 590			
214	ctc att ctc gag tac aga aag atc cag aaa ctg aaa tcg acc tac ata	1824		
215	Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile			
216	595 600 605			
218	gac acc ctt ccg aaa ctt gtg aac ccg aaa acc gga aga att cat gca	1872		
219	Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala			
220	610 615 620			
222	tct ttc cac cag acg ggt acc gcc act ggc agg ttg agt agc agt gat	1920		
223	Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp			
224	625 630 635 640			

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226 cca aat ctt cag aat ctt ccg aca aag agc gaa gag gga aaa gaa att      1968
227 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
228          645          650          655
230 aga aaa gcg att gtg ccc cag gat cca gac tgg tgg atc gtc agt gcg      2016
231 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
232          660          665          670
234 gat tat tcc caa ata gaa ctc aga atc ctc gct cat ctc agt ggt gat      2064
235 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
236          675          680          685
238 gag aac ctt gtg aag gcc ttc gag gag ggc atc gat gtg cac acc ttg      2112
239 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
240          690          695          700
242 act gcc tcc agg atc tac aac gta aag cca gaa gaa gtg aac gaa gaa      2160
243 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
244 705          710          715          720
246 atg cga cgg gtt gga aag atg gtg aac ttc tct ata ata tac ggt gtc      2208
247 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
248          725          730          735
250 aca ccg tac ggt ctt tct gtg aga ctt gga ata ccg gtt aaa gaa gca      2256
251 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
252          740          745          750
254 gaa aag atg att atc agc tat ttc aca ctg tat cca aag gtg cga agc      2304
255 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
256          755          760          765
258 tac atc cag cag gtt gtt gca gag gca aaa gag aag ggc tac gtc agg      2352
259 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
260          770          775          780
262 act ctc ttt gga aga aaa aga gat att ccc cag ctc atg gca agg gac      2400
263 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
264 785          790          795          800
266 aag aac acc cag tcc gaa ggc gaa aga atc gca ata aac acc ccc att      2448
267 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
268          805          810          815
270 cag gga acg gcg gca gat ata ata aaa ttg gct atg ata gat ata gac      2496
271 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
272          820          825          830
274 gag gag ctg aga aaa aga aac atg aaa tcc aga atg atc att cag gtt      2544
275 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
276          835          840          845
278 cat gac gaa ctg gtc ttc gag gtt ccc gat gag gaa aaa gaa gaa cta      2592
279 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
280          850          855          860
282 gtt gat ctg gtg aag aac aaa atg aca aat gtg gtg aaa ctc tct gtg      2640
283 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
284 865          870          875          880
286 cct ctt gag gtt gac ata agc atc gga aaa agc tgg tct tga      2682
287 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
288          885          890
291 <210> SEQ ID NO: 2

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293 <211> LENGTH: 893

295 <212> TYPE: PRT

297 <213> ORGANISM: Thermotoga neapolitana

301 <400> SEQUENCE: 2

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311 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
312 35 40 45
315 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
316 50 55 60
319 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Ala Tyr Lys Ala Gln Arg
320 65 70 75 80
323 Pro Lys Thr Pro Asp Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
324 85 90 95
327 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
328 100 105 110
331 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Cys Thr Phe Phe
332 115 120 125
335 Asp Glu Ile Phe Ile Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
336 130 135 140
339 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
340 145 150 155 160
343 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
344 165 170 175
347 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn
348 180 185 190
351 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
352 195 200 205
355 Gly Lys Tyr Arg Asn Leu Glu Asp Ile Leu Glu His Ala Arg Glu Leu
356 210 215 220
359 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
360 225 230 235 240
363 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
364 245 250 255
367 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
368 260 265 270
371 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
372 275 280 285
375 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
376 290 295 300
379 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
380 305 310 315 320
383 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
384 325 330 335
387 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
388 340 345 350
391 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser

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VERIFICATION SUMMARY

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